Amendments to the Specification

Please delete the paragraph on page 12, lines 6-13, of the originally filed specification, and replace it with the following new paragraph.

Protein identification based on mass spectrum data was carried out using the ProFound program (Zhang W and Chait BT. 2000. ProFound: an expert system for protein identification using mass spectrometric peptide mapping information. Anal Chem 72:2482-2489. ~~http://prowl.rockefeller.edu/cgi-bin/ProFound~~). The search was subscribed to the genes and derived protein sequences contained in the SwissProt database (~~http://www.ebi.ac.uk/swissprot/~~) and NCBI (~~http://www.ncbi.nlm.nih.gov/~~), considering the oxidation of methionines, deamidation and carboxyamidomethylation of cysteines as possible modifications to be encountered.

Please delete the paragraph on page 12, lines 14-18, of the originally filed specification, and replace it with the following new paragraph.

Identification of proteins based on the mass spectra was carried out with the MASCOT program (Perkins DN, et al. 1999. Probability-based protein identification by searching sequence databases using mass spectrometry data. Electrophoresis 20:3551-3567. ~~http://www.matrixscience.com/~~). Search parameters included cysteine modifications as well as oxidations and deamidations.

Please delete the paragraph starting on page 12, line 27, and ending on page 13, line 2, of the originally filed specification, and replace it with the following new paragraph.

For the identification of the NMB0928 protein, a sequence homology search was done in the NCBI data base employing the BLAST program (Altschul SF, et al. 1990. Basic local alignment search tool. J Mol Biol 215:403-410~~, http://www.ncbi.nlm.nih.gov/BLAST/~~). The results of this procedure indicated homology with, in addition to the corresponding protein in other serogroups of Neisseria, with the one in several microorganisms, including lipoprotein - 34 codified by the nlpB gene from Escherichia coli, identified in 1991. It is demonstrated that this protein is fractionated in the outer membrane proteoliposomes (Bouvier J, Pugsley A.P and Stragier,P. 1991. A gene for new lipoprotein in the dapA-purC interval of the E. coli chromosome. J Bacteriol 173(17):5523-31)

Please delete the paragraph starting on page 14, lines 4-5 of the originally filed specification, and replace it with the following new paragraph.

For the prediction of signal peptide the SignalP World Wide Web server ~~(http://www.ebs.dtu.dk/services/SignalP-2.0)~~ was employed.

Please delete the paragraph starting on page 16, lines 19-34 of the originally filed specification, and replace it with the following new paragraph.

To analyze the conservation of the sequence of the gene codifying for the NMB0928 protein in the pathogenic species of the Neisseria genus a similarity search with the genomes of Neisseria meningitidis (serogroups A, B and C) and Neisseria gonorrhoeae, annotated in the NCBI data base, was done (NC_003116.1, NC_003112.1, NC_003221, NC_002946 SANGER_135720|Contig1) employing the BLAST program (Altschul SF, et al. 1990. Basic local alignment search tool. J Mol Biol 215:403-410. ~~http://www.ncbi.nlm.nih.gov/BLAST/~~). Figure 8 shows the results of the sequence comparison for those sequences that produce a significant aligment in each of the analyzed genomes. Those sequences have 98% identity in serogroups A and C, 99% identity in serogroup B and 96%identity with Neisseria gonorrhoeae, with the sequence obtained for the gene that codicies for the NMB0928 protein (Seq. ID. No. 3). In addition, the sequence of the referred gene was determined for 3 Cuban isolates (Seq. ID. No. 5-7), which belong to serogroup B (B:4:P1.19,15) and a sequence alignment was done by using the ClustalX program (~~http://www.ebi.ac.uk/clustalw/~~). The results of the alignment show that there is a great conservation in the nucleotide sequence of the gene NMB0928 among the analyzed strains.